

SEQUENCE LISTING

<110> NATIONAL INSTITUTE OF ADVANCED INDUSTRIAL SCIENCE AND TECHNOLOGY
AMERSHAM BIOSCIENCES K.K.

<120> METHOD OF DETECTING BONE PAGET' S DISEASE

<130> YCT-882

<150> JP2002-323438

<151> 2002-11-07

<160> 70

<170> PatentIn version 3.1

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Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg Arg Pro Asn Ser
50 55 60

Val Gln Pro Gly Ala Glu Arg Glu Lys Pro Gly Ala Gly Glu Gly Ala
65 70 75 80

Gly Glu Asn Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro
85 90 95

Gly Gln Ala Ala Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu
100 105 110

Leu Gly Ile Arg Gln Arg Leu Leu Val Ala Val Leu Thr Ser Gln Thr
115 120 125

Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg
130 135 140

Leu Glu Arg Val Val Phe Leu Thr Gly Ala Arg Gly Arg Arg Ala Pro

145	150	155	160
Pro Gly Met Ala Val Val Thr Leu Gly Glu Glu Arg Pro Ile Gly His			
	165	170	175
Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe			
	180	185	190
Asp Trp Phe Phe Leu Val Pro Asp Thr Thr Tyr Thr Glu Ala His Gly			
	195	200	205
Leu Ala Arg Leu Thr Gly His Leu Ser Leu Ala Ser Ala Ala His Leu			
	210	215	220
Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Glu Pro Thr Pro Gly			
225		230	235 240
Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Met Leu Leu			
	245	250	255
Gln Gln Leu Arg Pro His Leu Glu Gly Cys Arg Asn Asp Ile Val Ser			
	260	265	270
Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly			
	275	280	285
Val Gly Cys Thr Gly Asp His Glu Gly Val His Tyr Ser His Leu Glu			
290		295	300

Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro His Phe Arg Ser
305 310 315 320

Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu
325 330 335

His Lys Ala Phe Ala Arg Ala Glu Leu Glu Arg Thr Tyr Gln Glu Ile
340 345 350

Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser His Leu Ala Val Asp
355 360 365

Gly Asp Arg Ala Ala Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg
370 375 380

Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln
385 390 395 400

His Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly
405 410 415

Ala Asp Arg Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu
420 425 430

Leu Asn Arg Arg Tyr His Pro Ala Leu Arg Leu Gln Lys Gln Gln Leu
435 440 445

Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr
450 455 460

Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Arg Pro
465 470 475 480

Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile
485 490 495

Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu
500 505 510

Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Pro Gly Phe Leu Glu Ala
515 520 525

Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Ala Ala Leu Thr
530 535 540

Leu Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Val Ala His Ala
545 550 555 560

Asp Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg
565 570 575

Phe Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro
580 585 590

Ser Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp
595 600 605

Thr Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe
610 615 620

Leu Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe
625 630 635 640

Pro Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly
645 650 655

Pro Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly Arg Phe Asp Arg Gln
660 665 670

Ala Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg
675 680 685

Gly Arg Leu Ala Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser
690 695 700

Leu Asp Val Tyr Glu Leu Phe Leu His Phe Ser Ser Leu His Val Leu
705 710 715 720

Arg Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Thr Cys
725 730 735

Ser Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Leu Gln Ser Val

740

745

750

Leu Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu
 755 760 765

Gln Glu Gln Gly Asn Ser Thr
 770 775

<210> 5
 <211> 1669
 <212> DNA
 <213> Homo sapiens

<220>
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 Met Phe Pro Ser Arg
 1 5
 agg aaa gcg gcg cag ctg ccc tgg gag gac ggc agg tcc ggg ttg ctc 103
 Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly Arg Ser Gly Leu Leu
 10 15 20
 tcc ggc ggc ctc cct cgg aag tgt tcc gtc ttc cac ctg ttc gtg gcc 151
 Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe His Leu Phe Val Ala
 25 30 35
 tgc ctc tcg ctg ggc ttc ttc tcc cta ctc tgg ctg cag ctc agc tgc 199
 Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp Leu Gln Leu Ser Cys
 40 45 50
 tct ggg gac gtg gcc cgg gca gtc agg gga caa ggg cag gag acc tcg 247
 Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln Gly Gln Glu Thr Ser
 55 60 65

ggc cct ccc cgc gcc tgc ccc cca gag cgc ccc cct gag cac tgg gaa	295
Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro Pro Glu His Trp Glu	
70 75 80 85	
gaa gac gca tcc tgg ggc ccc cac cgc ctg gca gtg ctg gtg ccc ttc	343
Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala Val Leu Val Pro Phe	
90 95 100	
cgc gaa cgc ttc gag gag ctc ctg gtc ttc gtg ccc cac atg cgc cgc	391
Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg	
105 110 115	
ttc ctg agc agg aag aag atc cgg cac cac atc tac gtg ctc aac cag	439
Phe Leu Ser Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln	
120 125 130	
gtg gac cac ttc agg ttc aac cgg gca gcg ctc atc aac gtg ggc ttc	487
Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe	
135 140 145	
ctg gag agc agc aac agc acg gac tac att gcc atg cac gac gtt gac	535
Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala Met His Asp Val Asp	
150 155 160 165	
ctg ctc cct ctc aac gag gag ctg gac tat ggc ttt cct gag gct ggg	583
Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly Phe Pro Glu Ala Gly	
170 175 180	
ccc ttc cac gtg gcc tcc ccg gag ctc cac cct ctc tac cac tac aag	631
Pro Phe His Val Ala Ser Pro Glu Leu His Pro Leu Tyr His Tyr Lys	
185 190 195	
acc tat gtc ggc ggc atc ctg ctg ctc tcc aag cag cac tac cgg ctg	679
Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys Gln His Tyr Arg Leu	
200 205 210	
tgc aat ggg atg tcc aac cgc ttc tgg ggc tgg ggc cgc gag gac gac	727
Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp Gly Arg Glu Asp Asp	
215 220 225	
gag ttc tac cgg cgc att aag gga gct ggg ctc cag ctt ttc cgc ccc	775
Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu Gln Leu Phe Arg Pro	
230 235 240 245	
tcg gga atc aca act ggg tac aag aca ttt cgc cac ctg cac gac cca	823
Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg His Leu His Asp Pro	
250 255 260	
gcc tgg cgg aag agg gac cag aag cgc atc gca gct caa aaa cag gag	871

Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala Ala Gln Lys Gln Glu	
265 270 275	
cag ttc aag gtg gac agg gag gga ggc ctg aac act gtg aag tac cat	919
Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn Thr Val Lys Tyr His	
280 285 290	
gtg gct tcc cgc act gcc ctg tct gtg ggc ggg gcc ccc tgc act gtc	967
Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly Ala Pro Cys Thr Val	
295 300 305	
ctc aac atc atg ttg gac tgt gac aag acc gcc aca ccc tgg tgc aca	1015
Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala Thr Pro Trp Cys Thr	
310 315 320 325	
ttc agc tga gctggatgga cagtgaggaa gccctgtacct acaggccata	1064
Phe Ser	
ttgtctaggc tcaggacaag gccctcaggtc gtggggcccag ctctgacagg atgtggagtg	1124
gccaggacca agacagcaag ctacgcaatt gcagccaccc ggccgccaag gcaggcttgg	1184
gctggggccag gacacgtggg gtgcttggga cgtctgttgc catgcacagt gatcagagag	1244
aggctgggggt gtgtcctgtc cgggaccccc cctgccttcc tgcctaccct actctgacct	1304
cccttcacgtg cccaggcctg tgggtagtgg ggagggctga acaggacaac ctcctatcac	1364
ccccactiit gtctcttccct gctgggctgc ctctgtcaga gacacagtgt aggggccaatg	1424
cagctggcgt aggtggcagt igggccctgt gagggctagg acttcagaaa ccagagcaca	1484
agccccacag agggggaaca gccagcaccg ctctagcttg ttgttgccat gccggaatgt	1544
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gtgatatctt ctgatttttt aaatgatagc acctaaatga aactttcaaa aagtaaaaaa	1664
aaaaa	1669

<210> 6
 <211> 327
 <212> PRT
 <213> Homo sapiens

<400> 6

Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly
1 5 10 15

Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser Val Phe

20

25

30

His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser Leu Leu Trp
 35 40 45

Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala Val Arg Gly Gln
 50 55 60

Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
 65 70 75 80

Pro Glu His Trp Glu Glu Asp Ala Ser Trp Gly Pro His Arg Leu Ala
 85 90 95

Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
 100 105 110

Pro His Met Arg Arg Phe Leu Ser Arg Lys Lys Ile Arg His His Ile
 115 120 125

Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu
 130 135 140

Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
 145 150 155 160

Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
 165 170 175

Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
180 185 190

Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
195 200 205

Gln His Tyr Arg Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
210 215 220

Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
225 230 235 240

Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Lys Thr Phe Arg
245 250 255

His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
260 265 270

Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
275 280 285

Thr Val Lys Tyr His Val Ala Ser Arg Thr Ala Leu Ser Val Gly Gly
290 295 300

Ala Pro Cys Thr Val Leu Asn Ile Met Leu Asp Cys Asp Lys Thr Ala
305 310 315 320

Thr Pro Trp Cys Thr Phe Ser
325

<210> 7
<211> 26
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR (K3)

<400> 7
cccaagcttg ccgaggggga gcccga 26

<210> 8
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR (K3)

<400> 8
gctctagact gtcaggagag agttcgatt 29

<210> 9
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR (K3)

<400> 9
atggctgtgc gctctcgccg cccgt 25

<210> 10
<211> 25
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR (K3)

<400> 10
cgccccgct gccgttgigg ctact

25

<210> 11
<211> 25
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR (K3)

<400> 11
agtagccaca acggcagcgg ggacg

25

<210> 12
<211> 24
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR (K3)

<400> 12
tcaggagaga gttcgattgt acct

24

<210> 13
<211> 28
<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR (K11)

<400> 13

ggaattccgg ccaggccgcc aaaaaggc

28

<210> 14

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR (K11)

<400> 14

cgggatccic aggtgctgtt gccctgtcc

30

<210> 15

<211> 16

<212> PRT

<213> Artificial

<220>

<223> Description of Artificial Sequence: synthesised substance for assay

<400> 15

Val Leu Pro Gln Glu Glu Glu Gly Ser Gly Gly Gly Gln Leu Val Thr

1

5

10

15

<210> 16

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K3 exon 1)

<400> 16

cgacagccca gcgagcgtcc

20

<210> 17

<211> 22

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K3 exon 1)

<400> 17

ggagactggc aggctggaaa gc

22

<210> 18

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 1)

<400> 18

agggggagcc cgaggaggag

20

<210> 19

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 1)

<400> 19

ctcctcctcg ggctccccct

20

<210> 20

<211> 27

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K3 exon 2)

<400> 20

gagacatagt aattgttgcc tttcttt

27

<210> 21

<211> 25

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K3 exon 2)

<400> 21

gtgaacattt tcatcacagc tccat

25

<210> 22

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K3 exon 3)

<400> 22

tagatgcttt agtttatcgc tggttt

26

<210> 23

<211> 26

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K3 exon 3)

<400> 23

ttaaaaaagg caaaatgtgt tgcctg

26

<210> 24

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 24

tctatactca gcagctgaga acca

24

<210> 25

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 25

tggtttctcag ctgctgagta taga 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 26

gaaatgggag ggcacaatga aaag 24

<210> 27

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 27

cttttcattg tgccctccca ttcc 24

<210> 28

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

n 3)

<400> 28

tagccagiat gacccaaagg taac

24

<210> 29

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 29

gttaccttgg ggtcatactg gcta

24

<210> 30

<211> 31

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 30

aggccattca gaagccaaga agtaggagtg g

31

<210> 31

<211> 31

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K3 exon 3)

<400> 31
ccactccctac ttcttggctt ctgaatggcc t 31

<210> 32
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 1)

<400> 32
tcggagactc ctctggctgc t 21

<210> 33
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 1)

<400> 33
tagagcgggc gcagccgac a 21

<210> 34
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 2)

<400> 34
tttgataagc ttgtgccatc tcctc 25

<210> 35
<211> 25
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 2)

<400> 35
aggtatcagt gggatagctt atcat 25

<210> 36
<211> 24
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 3)

<400> 36
agctcatcac agatcccttc cctt 24

<210> 37
<211> 22
<212> DNA
<213> Artificial

<220>
<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 1)

<400> 37

actctgccac ccccagacct ag

22

<210> 38

<211> 24

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (K11 exon 4)

<400> 38

ttgctgatgg cctgtttctc tgat

24

<210> 39

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (K11 exon 4)

<400> 39

gtgtggccat gccacggccc a

21

<210> 40

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K11 exon 4)

<400> 40

tatgtcacig aggcctcacg tct

23

<210> 41
<211> 23
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K11 exon 4)

<400> 41
agacgtgagg cctcagtgac ata

23

<210> 42
<211> 24
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: primer for sequencing (K11 exon 4)

<400> 42
atgcatttcc aagccttcca ccca

24

<210> 43
<211> 24
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: Primer for sequencing (K11 exon 4)

<400> 43
tgggtggaag gcttggaaat gcat

24

<210> 44
<211> 20
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 1)

<400> 44
tgcgagcgcc tgcccatgc 20

<210> 45
<211> 22
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 1)

<400> 45
gatggcctcg ggttcccaga tt 22

<210> 46
<211> 21
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 2)

<400> 46
tcctgaccct gtcccgcgct t 21

<210> 47

<211> 20
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 2)

<400> 47
aggggtgccg aggggagagg

20

<210> 48
<211> 21
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 3)

<400> 48
ctgcccagcc ttgcccaccc t

21

<210> 49
<211> 22
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 3)

<400> 49
gctctgagca gagcaggctg tc

22

<210> 50
<211> 22

<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 4)

<400> 50
agatgggccg agtgacgctg ct 22

<210> 51
<211> 21
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 4)

<400> 51
ctcagggcag ccaccgcagc t 21

<210> 52
<211> 22
<212> DNA
<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 5)

<400> 52
aagggcagcc tgaccccgac tt 22

<210> 53
<211> 23
<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 5)

<400> 53

atgaccacct atccgtcccc aat

23

<210> 54

<211> 22

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for PCR and sequencing (beta4Gal-T7 exon 6)

<400> 54

cagccctgag tccgtgctct tt

22

<210> 55

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 6)

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<221> misc_feature

<223> Description of Artificial Sequence: 3' primer for PCR and sequencing (beta4Gal-T7 exon 6)

<400> 55

tgccctglag gtacaggctt cct

23

<210> 56

<211> 23

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for RT-PCR (K3)

<400> 56

cccagaaaaa gtccttcacg atg

23

<210> 57

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for RT-PCR (K3)

<400> 57

aactcttcta attgtcacc ttgatgtag

30

<210> 58

<211> 17

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Probe for RT-PCR (K3)

<400> 58

atgagtgggt catgcgc

17

<210> 59

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for RT-PCR (K11)

<400> 59

gctgaactgg aacgcacgta

20

<210> 60

<211> 19

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for RT-PCR (K11)

<400> 60

cgggatggig ctggaatac

19

<210> 61

<211> 20

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Probe for RT-PCR (K11)

<400> 61

agatccagga gttacagtgg

20

<210> 62

<211> 18

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 5' primer for RT-PCR (beta4Gal-T7)

<400> 62

cggcgcatla agggagct

18

<210> 63

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: 3' primer for RT-PCR (beta4Gal-T7)

<400> 63

tacccagttg tgattcccga g

21

<210> 64

<211> 14

<212> DNA

<213> Artificial

<220>

<223> Description of Artificial Sequence: Probe for RT-PCR (beta4Gal-T7)

<400> 64

ctccagcttt tccg

14

<210> 65

<211> 2652

<212> DNA

<213> mouse

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gtc ctg ggc ttc acc gcc gcg tcc tgg ctc atc gcc ccc cgg gtg gcc	96
Val Leu Gly Phe Thr Ala Ala Ser Trp Leu Ile Ala Pro Arg Val Ala	
20 25 30	
gag ctg agc gag aag agg cga cgc ggc tcc agt ctt tgc tcc tac tac	144
Glu Leu Ser Glu Lys Arg Arg Arg Gly Ser Ser Leu Cys Ser Tyr Tyr	
35 40 45	
ggc cgc tcg gct acc ggg ccc cgc gcg gac gcg cag cag ctg ctc ccc	192
Gly Arg Ser Ala Thr Gly Pro Arg Ala Asp Ala Gln Gln Leu Leu Pro	
50 55 60	
caa ccc cag tcc cgg ccg cgg cta gag cag tcg ccg ccc cct gcc agc	240
Gln Pro Gln Ser Arg Pro Arg Leu Glu Gln Ser Pro Pro Pro Ala Ser	
65 70 75 80	
cac gag ctc ccc ggt cct cag cag ccg gag gcg gcg ccc gga ggt ccc	288
His Glu Leu Pro Gly Pro Gln Gln Pro Glu Ala Ala Pro Gly Gly Pro	
85 90 95	
agt ttt cgg agc agc ccc tgg cag cag ccg gct ctg ttg ccg cag agg	336
Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Ala Leu Leu Pro Gln Arg	
100 105 110	
agg cga gga cac acg ccc gaa ggt gcg acg gcg ctt ccc ggc gct ccg	384
Arg Arg Gly His Thr Pro Glu Gly Ala Thr Ala Leu Pro Gly Ala Pro	
115 120 125	
gct gcc aaa ggg gaa cca gag gag gag gat ggg ggc gcg gct gac cct	432
Ala Ala Lys Gly Glu Pro Glu Glu Glu Asp Gly Gly Ala Ala Asp Pro	
130 135 140	
cgg aag ggt ggc cgg ccg ggg agc agc cac aac ggc agc ggg gac ggg	480
Arg Lys Gly Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly	
145 150 155 160	
ggt gcc gct gtc ccg acc tcc gga ccc ggg gac ttc ctg tac gtg ggt	528
Gly Ala Ala Val Pro Thr Ser Gly Pro Gly Asp Phe Leu Tyr Val Gly	
165 170 175	

gtg atg acc gca cag aag tac ctg ggc agt cgc gcg ctg gcc gcg cag	576
Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln	
180 185 190	
cgg acc tgg gcg cgc ttc atc cct ggc cgc gtg gag ttc ttt tcc agt	624
Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser	
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cag caa tct ccc agt gct gcg ctt ggc cag ccc ccg cca cct ttg cct	672
Gln Gln Ser Pro Ser Ala Ala Leu Gly Gln Pro Pro Pro Pro Leu Pro	
210 215 220	
gtc atc gcg ctg cca ggg gtc gac gat tcc tac cct ccc cag aaa aag	720
Val Ile Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys	
225 230 235 240	
tcc ttc atg atg atc aag tac atg cac gac cac tat ctg gac aag tat	768
Ser Phe Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr	
245 250 255	
gag igg ttc atg cgc gcc gac gac gat gtc tac atc aaa ggt gat aag	816
Glu Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Lys	
260 265 270	
tta gaa gaa ttt cta aga tcc cta aat agc agc aag cct ctc tac ctg	864
Leu Glu Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu	
275 280 285	
gga cag acg ggc ctg ggc aat act gaa gaa ctt gga aag ctg ggg ctg	912
Gly Gln Thr Gly Leu Gly Asn Thr Glu Glu Leu Gly Lys Leu Gly Leu	
290 295 300	
gag ccc ggg gag aac ttc tgc atg gga gga cct ggc atg atc ttc agc	960
Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser	
305 310 315 320	
aga gag gtt ctc agg cgg atg gtg cct cat atc ggc gaa tgc ctc cga	1008
Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg	
325 330 335	
gag atg tac acc aca cac gaa gac gta gaa gta gga agg tgt gtt cgc	1056
Glu Met Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg	
340 345 350	
cgt ttc ggc ggg acg cag tgt gtc tgg tct tat gag atg cag cag ctg	1104
Arg Phe Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu	
355 360 365	
ttc cat gaa aac tac gaa cac aat cgc aag ggt tac atc caa gac ctc	1152

Phe	His	Glu	Asn	Tyr	Glu	His	Asn	Arg	Lys	Gly	Tyr	Ile	Gln	Asp	Leu		
370						375					380						
cac	aac	agc	aaa	atc	cac	gca	gcc	atc	acg	ctc	cat	ccg	aac	aaa	agg	1200	
His	Asn	Ser	Lys	Ile	His	Ala	Ala	Ile	Thr	Leu	His	Pro	Asn	Lys	Arg		
385					390					395					400		
ccc	gcg	tac	cag	tac	aga	ctt	cat	aac	tac	atg	ctc	agc	cgc	aag	atc	1248	
Pro	Ala	Tyr	Gln	Tyr	Arg	Leu	His	Asn	Tyr	Met	Leu	Ser	Arg	Lys	Ile		
				405						410					415		
tcc	gag	ctc	cgc	tac	cgc	acc	atc	cag	ctc	cac	cgg	gag	agc	gct	ctc	1296	
Ser	Glu	Leu	Arg	Tyr	Arg	Thr	Ile	Gln	Leu	His	Arg	Glu	Ser	Ala	Leu		
				420						425					430		
atg	agc	aag	ctc	agc	aac	agt	gaa	gtg	agc	aaa	gag	gac	caa	cag	ctg	1344	
Met	Ser	Lys	Leu	Ser	Asn	Ser	Glu	Val	Ser	Lys	Glu	Asp	Gln	Gln	Leu		
				435						440					445		
gga	agg	acg	ccg	tcc	ttc	aac	cac	ttc	cag	cct	cgg	gag	aga	aat	gaa	1392	
Gly	Arg	Thr	Pro	Ser	Phe	Asn	His	Phe	Gln	Pro	Arg	Glu	Arg	Asn	Glu		
				450						455					460		
gtc	atg	gag	tgg	gag	ttc	ctg	acg	ggg	aag	ctg	cit	tac	tca	gct	gca	1440	
Val	Met	Glu	Trp	Glu	Phe	Leu	Thr	Gly	Lys	Leu	Leu	Tyr	Ser	Ala	Ala		
465					470					475					480		
gag	aac	cag	cct	cct	cga	cag	agc	atc	aac	agc	atc	cta	agg	tca	gct	1488	
Glu	Asn	Gln	Pro	Pro	Arg	Gln	Ser	Ile	Asn	Ser	Ile	Leu	Arg	Ser	Ala		
				485						490					495		
ctg	gat	gac	act	gtc	ctg	cag	gtg	atg	gag	atg	atc	aac	gag	aat	gcc	1536	
Leu	Asp	Asp	Thr	Val	Leu	Gln	Val	Met	Glu	Met	Ile	Asn	Glu	Asn	Ala		
				500						505					510		
aag	agt	agg	ggc	cga	ctc	atc	gac	ttc	aag	gaa	att	cag	tat	ggc	tac	1584	
Lys	Ser	Arg	Gly	Arg	Leu	Ile	Asp	Phe	Lys	Glu	Ile	Gln	Tyr	Gly	Tyr		
				515						520					525		
cgc	agg	gtt	gat	ccc	atg	cac	ggg	gtt	gag	tac	ata	tig	gac	ctg	cta	1632	
Arg	Arg	Val	Asp	Pro	Met	His	Gly	Val	Glu	Tyr	Ile	Leu	Asp	Leu	Leu		
				530						535					540		
ctc	ctg	tac	aaa	agg	cac	aaa	gga	agg	aaa	ctg	act	gtg	cct	gtg	agg	1680	
Leu	Leu	Tyr	Lys	Arg	His	Lys	Gly	Arg	Lys	Leu	Thr	Val	Pro	Val	Arg		
545					550					555					560		
cgc	cat	gcc	tat	cit	cag	cag	cca	ttt	agc	aag	cct	ttc	ttc	aga	gag	1728	
Arg	His	Ala	Tyr	Leu	Gln	Gln	Pro	Phe	Ser	Lys	Pro	Phe	Phe	Arg	Glu		

565	570	575	
gtg gaa gaa ctc gac gtc aac cgt ctg gtg gag agt atc aac agc ggt			1776
Val Glu Glu Leu Asp Val Asn Arg Leu Val Glu Ser Ile Asn Ser Gly			
580	585	590	
aca cag tca ttc tcc gtt ata tcc aat tct cta aaa att ctc tct tct			1824
Thr Gln Ser Phe Ser Val Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser			
595	600	605	
ctt caa gag gcc aaa gac ata gga ggg cac aat gaa aag aaa gta cac			1872
Leu Gln Glu Ala Lys Asp Ile Gly Gly His Asn Glu Lys Lys Val His			
610	615	620	
att ctc gtt cca ctc gtt gga agg tac gac att ttc ttg aga ttc atg			1920
Ile Leu Val Pro Leu Val Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met			
625	630	635	640
gaa aat ttt gaa agt acg tgt ctt atc cca aag caa aat gtc aag ctt			1968
Glu Asn Phe Glu Ser Thr Cys Leu Ile Pro Lys Gln Asn Val Lys Leu			
645	650	655	
gtc atc atc ctt ttc agc agg gat gct ggc caa gag tcc atc aag cac			2016
Val Ile Ile Leu Phe Ser Arg Asp Ala Gly Gln Glu Ser Ile Lys His			
660	665	670	
att gag ctg ata caa gaa tat cag agc agg tat ccc agt gca gaa atg			2064
Ile Glu Leu Ile Gln Glu Tyr Gln Ser Arg Tyr Pro Ser Ala Glu Met			
675	680	685	
atg ctc att ccc atg aag gga gag ttt tcc aga ggt ctt ggt ctt gaa			2112
Met Leu Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu			
690	695	700	
atg gct tct tcc cag ttt gac aat gac aca ttg ctg cta ttt tgt gat			2160
Met Ala Ser Ser Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp			
705	710	715	720
gtt gac ttg att ttc aga gga gac ttc ctc caa cgc tgt cga gac aat			2208
Val Asp Leu Ile Phe Arg Gly Asp Phe Leu Gln Arg Cys Arg Asp Asn			
725	730	735	
aca gtt cag gga caa cag gta tat tac ccc atc atc ttt agc cag tat			2256
Thr Val Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr			
740	745	750	
gac cca aag gtc acc cat atg aga aat cct ccc aca gag ggt gac ttt			2304
Asp Pro Lys Val Thr His Met Arg Asn Pro Pro Thr Glu Gly Asp Phe			
755	760	765	

gta ttc tca aag gaa act ggg ttt tgg aga gac tat ggc tac gga atc	2352
Val Phe Ser Lys Glu Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile	
770 775 780	
aca tgc att tac aaa agc gat cta ctg ggt gca ggt gga ttt gat acc	2400
Thr Cys Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr	
785 790 795 800	
tca ata caa ggc tgg gga ctg gaa gat gta gat ctc tat aat aaa gtc	2448
Ser Ile Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val	
805 810 815	
atc cta tct ggc tta cgg ccc ttc aga agt caa gaa gtg gga gtg gtg	2496
Ile Leu Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val	
820 825 830	
cat att ttc cat cct gtt cat tgt gat cct aac ttg gac cct aag cag	2544
His Ile Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln	
835 840 845	
tat aag atg tgc tta gga tcc aaa gca agt act ttt gcc tca acc atg	2592
Tyr Lys Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met	
850 855 860	
caa ctg gct gaa ctc tgg tta gaa aaa cat ttg ggt gtc agg gat aat	2640
Gln Leu Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Asp Asn	
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cga act ctc tcc	2652
Arg Thr Leu Ser	

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35 40 45

Gly Arg Ser Ala Thr Gly Pro Arg Ala Asp Ala Gln Gln Leu Leu Pro
50 55 60

Gln Pro Gln Ser Arg Pro Arg Leu Glu Gln Ser Pro Pro Pro Ala Ser
65 70 75 80

His Glu Leu Pro Gly Pro Gln Gln Pro Glu Ala Ala Pro Gly Gly Pro
85 90 95

Ser Phe Arg Ser Ser Pro Trp Gln Gln Pro Ala Leu Leu Pro Gln Arg
100 105 110

Arg Arg Gly His Thr Pro Glu Gly Ala Thr Ala Leu Pro Gly Ala Pro
115 120 125

Ala Ala Lys Gly Glu Pro Glu Glu Glu Asp Gly Gly Ala Ala Asp Pro
130 135 140

Arg Lys Gly Gly Arg Pro Gly Ser Ser His Asn Gly Ser Gly Asp Gly
145 150 155 160

Gly Ala Ala Val Pro Thr Ser Gly Pro Gly Asp Phe Leu Tyr Val Gly
165 170 175

Val Met Thr Ala Gln Lys Tyr Leu Gly Ser Arg Ala Leu Ala Ala Gln
180 185 190

Arg Thr Trp Ala Arg Phe Ile Pro Gly Arg Val Glu Phe Phe Ser Ser
195 200 205

Gln Gln Ser Pro Ser Ala Ala Leu Gly Gln Pro Pro Pro Pro Leu Pro
210 215 220

Val Ile Ala Leu Pro Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys
225 230 235 240

Ser Phe Met Met Ile Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr
245 250 255

Glu Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Lys
260 265 270

Leu Glu Glu Phe Leu Arg Ser Leu Asn Ser Ser Lys Pro Leu Tyr Leu
275 280 285

Gly Gln Thr Gly Leu Gly Asn Thr Glu Glu Leu Gly Lys Leu Gly Leu
290 295 300

Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Met Ile Phe Ser
305 310 315 320

Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly Glu Cys Leu Arg
325 330 335

Glu Met Tyr Thr Thr His Glu Asp Val Glu Val Gly Arg Cys Val Arg
340 345 350

Arg Phe Gly Gly Thr Gln Cys Val Trp Ser Tyr Glu Met Gln Gln Leu
355 360 365

Phe His Glu Asn Tyr Glu His Asn Arg Lys Gly Tyr Ile Gln Asp Leu
370 375 380

His Asn Ser Lys Ile His Ala Ala Ile Thr Leu His Pro Asn Lys Arg
385 390 395 400

Pro Ala Tyr Gln Tyr Arg Leu His Asn Tyr Met Leu Ser Arg Lys Ile
405 410 415

Ser Glu Leu Arg Tyr Arg Thr Ile Gln Leu His Arg Glu Ser Ala Leu
420 425 430

Met Ser Lys Leu Ser Asn Ser Glu Val Ser Lys Glu Asp Gln Gln Leu
435 440 445

Gly Arg Thr Pro Ser Phe Asn His Phe Gln Pro Arg Glu Arg Asn Glu
450 455 460

Val Met Glu Trp Glu Phe Leu Thr Gly Lys Leu Leu Tyr Ser Ala Ala

465 470 475 480

Glu Asn Gln Pro Pro Arg Gln Ser Ile Asn Ser Ile Leu Arg Ser Ala
 485 490 495

Leu Asp Asp Thr Val Leu Gln Val Met Glu Met Ile Asn Glu Asn Ala
 500 505 510

Lys Ser Arg Gly Arg Leu Ile Asp Phe Lys Glu Ile Gln Tyr Gly Tyr
 515 520 525

Arg Arg Val Asp Pro Met His Gly Val Glu Tyr Ile Leu Asp Leu Leu
 530 535 540

Leu Leu Tyr Lys Arg His Lys Gly Arg Lys Leu Thr Val Pro Val Arg
545 550 555 560

Arg His Ala Tyr Leu Gln Gln Pro Phe Ser Lys Pro Phe Phe Arg Glu
 565 570 575

Val Glu Glu Leu Asp Val Asn Arg Leu Val Glu Ser Ile Asn Ser Gly
 580 585 590

Thr Gln Ser Phe Ser Val Ile Ser Asn Ser Leu Lys Ile Leu Ser Ser
 595 600 605

Leu Gln Glu Ala Lys Asp Ile Gly Gly His Asn Glu Lys Lys Val His
 610 615 620

Ile Leu Val Pro Leu Val Gly Arg Tyr Asp Ile Phe Leu Arg Phe Met
625 630 635 640

Glu Asn Phe Glu Ser Thr Cys Leu Ile Pro Lys Gln Asn Val Lys Leu
 645 650 655

Val Ile Ile Leu Phe Ser Arg Asp Ala Gly Gln Glu Ser Ile Lys His
 660 665 670

Ile Glu Leu Ile Gln Glu Tyr Gln Ser Arg Tyr Pro Ser Ala Glu Met
 675 680 685

Met Leu Ile Pro Met Lys Gly Glu Phe Ser Arg Gly Leu Gly Leu Glu
 690 695 700

Met Ala Ser Ser Gln Phe Asp Asn Asp Thr Leu Leu Leu Phe Cys Asp
705 710 715 720

Val Asp Leu Ile Phe Arg Gly Asp Phe Leu Gln Arg Cys Arg Asp Asn
 725 730 735

Thr Val Gln Gly Gln Gln Val Tyr Tyr Pro Ile Ile Phe Ser Gln Tyr
 740 745 750

Asp Pro Lys Val Thr His Met Arg Asn Pro Pro Thr Glu Gly Asp Phe
 755 760 765

Val Phe Ser Lys Glu Thr Gly Phe Trp Arg Asp Tyr Gly Tyr Gly Ile
770 775 780

Thr Cys Ile Tyr Lys Ser Asp Leu Leu Gly Ala Gly Gly Phe Asp Thr
785 790 795 800

Ser Ile Gln Gly Trp Gly Leu Glu Asp Val Asp Leu Tyr Asn Lys Val
805 810 815

Ile Leu Ser Gly Leu Arg Pro Phe Arg Ser Gln Glu Val Gly Val Val
820 825 830

His Ile Phe His Pro Val His Cys Asp Pro Asn Leu Asp Pro Lys Gln
835 840 845

Tyr Lys Met Cys Leu Gly Ser Lys Ala Ser Thr Phe Ala Ser Thr Met
850 855 860

Gln Leu Ala Glu Leu Trp Leu Glu Lys His Leu Gly Val Arg Asp Asn
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Arg Thr Leu Ser

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Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr	
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tgg gtg gag gag cct tgc gga ccc ggg ccg ccc caa ccc gga gac tct	144
Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro Gly Asp Ser	
35 40 45	
gag ctg ccg ccg cgc ggc aac acc aac gcg gcg cgc cgg ccc aac tcg	192
Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg Arg Pro Asn Ser	
50 55 60	
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Val Gln Pro Gly Ser Glu Arg Glu Arg Pro Gly Ala Gly Ala Gly Thr	
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ggg gag agc tgg gag cct cgt gtc ttg ccc tac cat ccc gcg cag cca	288
Gly Glu Ser Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro	
85 90 95	
ggc cag gcc acc aag aag gcc gtc aga act cgg tat atc agc acg gag	336
Gly Gln Ala Thr Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu	
100 105 110	
ctg ggc atc agg cag aag ctt ctg gtg gca gtg ctg acc tca caa gcc	384
Leu Gly Ile Arg Gln Lys Leu Leu Val Ala Val Leu Thr Ser Gln Ala	
115 120 125	
acg ttg cct aca ctg ggt gtg gct gta aac cga act ctg gga cac cga	432
Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg	
130 135 140	
ctg gag cat gta gtg ttc ctg acc ggt gcg agg ggc cgc cgg aca cct	480
Leu Glu His Val Val Phe Leu Thr Gly Ala Arg Gly Arg Arg Thr Pro	
145 150 155 160	

tca ggc atg gcg gtg gtg gca ctg ggc gaa gag agg ccc atc gga cac	528
Ser Gly Met Ala Val Val Ala Leu Gly Glu Glu Arg Pro Ile Gly His	
165 170 175	
ctg cac ctg gcg ctg cgc cac ctg ctg gag caa cac ggc gat gac ttt	576
Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe	
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Asp Trp Phe Phe Leu Val Pro Asp Ala Thr Tyr Thr Glu Ala His Gly	
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ctg gac cgc cta gct ggc cac ctg agc ctt gct tca gca acc cat ctg	672
Leu Asp Arg Leu Ala Gly His Leu Ser Leu Ala Ser Ala Thr His Leu	
210 215 220	
tat ctt ggc cgg ccg cag gac ttc atc ggt gga gat act acc cca ggc	720
Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Asp Thr Thr Pro Gly	
225 230 235 240	
cgc tac tgc cac ggg ggc ttt gga gtc ttg ctg tct cgc aca ctg cta	768
Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Thr Leu Leu	
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Gln Gln Leu Arg Pro His Leu Glu Ser Cys Arg Asn Asp Ile Val Ser	
260 265 270	
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Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly	
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Val Gly Cys Thr Gly Asp His Glu Gly Met His Tyr Asn Tyr Leu Glu	
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ctg agc ccc ggg gag cct gta cag gag ggg gac cct cgt ttc cgc agc	960
Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro Arg Phe Arg Ser	
305 310 315 320	
gcc ttg aca gcc cat ccc gtg cgt gac cct gtg cac atg tac cag ctg	1008
Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu	
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cac aaa gct ttt gcc cgc gct gag ctg gac cgc acg tac cag gag att	1056
His Lys Ala Phe Ala Arg Ala Glu Leu Asp Arg Thr Tyr Gln Glu Ile	
340 345 350	
caa gaa ttg cag tgg gag atc cag aat acc agc cga ctg gct gct gat	1104

Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser Arg Leu Ala Ala Asp	
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365	
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Gly Glu Arg Ala Ser Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg	
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380	
cct gcc tca cgc ttt gag gtt ctg cgc tgg gac tac ttc aca gaa caa	1200
Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln	
385	390
395	400
tac gcg ttc tcc tgc gcc gat ggc tct ccc cgc tgc ccg ttg cgt ggg	1248
Tyr Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly	
405	410
415	
gcc gac cag gct gat gtg gct gac gtc ctg ggg aca gcc tta gag gag	1296
Ala Asp Gln Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu	
420	425
430	
ctc aac cgc cgt tac cag cca gcg ctg cag ctc cag aag caa cag ctg	1344
Leu Asn Arg Arg Tyr Gln Pro Ala Leu Gln Leu Gln Lys Gln Gln Leu	
435	440
445	
gtg aac ggc tac cgg cgt ttt gat cca gcc cga ggc atg gag tac aca	1392
Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr	
450	455
460	
cta gac ctg cag ctg gaa gcg ctg aca ccc cag ggt ggc cgc tgg ccc	1440
Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Trp Pro	
465	470
475	480
ctc acc cgc agg gtg cag ctc ctt cgg ccc ttg agc cga gtg gag atc	1488
Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile	
485	490
495	
ttg cct gta ccc tat gtc acc gag gct tct cgg ctc act gtg cta ctg	1536
Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu	
500	505
510	
ccg ctg gct gca gcg gaa cga gac ctg gct tct ggc ttc tta gaa gcc	1584
Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Ser Gly Phe Leu Glu Ala	
515	520
525	
ttt gcc act gca gcc ctg gaa cct ggt gat gca gca gcc ttg acc ctg	1632
Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Ala Leu Thr Leu	
530	535
540	
ctg ctg ctg tat gag cca cgc cag gcc cag cgg gca gcc cac tca gac	1680
Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Ala Ala His Ser Asp	

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gtc ttc gca cct gtc aag gcc cac gtg gca gag cta gag cgg cgt ttc				1728
Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg Phe				
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cct ggt gcc cgg gtg ccc tgg ctc agt gtg cag aca gca gcg ccc tct				1776
Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro Ser				
	580	585	590	
cca ctg cgt ctc atg gat ctg ctg tcc aag aag cac cca cta gac act				1824
Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp Thr				
	595	600	605	
ctg ttc ctg ctg gcc ggg cca gac acg gta ctc aca cct gat ttc ctg				1872
Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe Leu				
	610	615	620	
aac cgc tgc cgc atg cat gcc atc tct ggc tgg cag gcc ttc ttc ccc				1920
Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe Pro				
	625	630	635	640
atg cac ttc cag gcc ttc cac cct gct gtg gct cct cct cag ggc cct				1968
Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly Pro				
	645	650	655	
ggg cca cca gag ctg ggc cgt gac acc ggt cac ttt gat cgc cag gct				2016
Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly His Phe Asp Arg Gln Ala				
	660	665	670	
gcc agt gag gca tgc ttc tac aac tcc gac tat gtg gcg gcc cgt ggc				2064
Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg Gly				
	675	680	685	
cgg ctg gtg gcg gcc tcg gag cag gag gag gag ctg ctg gag agc ctg				2112
Arg Leu Val Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser Leu				
	690	695	700	
gat gtg tac gag ttg ttt ctg cgc ttc tcc aac ttg cac gtg ctg aga				2160
Asp Val Tyr Glu Leu Phe Leu Arg Phe Ser Asn Leu His Val Leu Arg				
	705	710	715	720
gca gta gag cca gcc ttg ctg cag cgc tac cgg gcc cag ccg tgc agt				2208
Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Pro Cys Ser				
	725	730	735	
gca cgg ctc agt gaa gac ctt tac cac cgc tgt cgc cag agc gta ctt				2256
Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Arg Gln Ser Val Leu				
	740	745	750	

gag ggc ctt ggc tcc cgc acc cag ctt gcc atg ctg ctc ttt gag cag 2304
 Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu Gln

755 760 765

gaa cag ggg aac agc acc taa gccccctgcac ctgtccctgc tcttccccag 2355
 Glu Gln Gly Asn Ser Thr

770

gaacctggag ccacgtgccca gcctcgtctgg acagggctgg ctgtagcctc agtcacctagg 2415

gcagcccact ggtcccttgt ctccttgcctt gtiggaccca tgggctcagg acaagccctg 2475

agacagatgc cctag 2490

<210> 68

<211> 774

<212> PRT

<213> mouse

<400> 68

Met Arg Ala Ser Leu Leu Leu Ser Val Leu Arg Pro Ala Gly Pro Val

1 5 10 15

Ala Val Gly Ile Ser Leu Gly Phe Thr Leu Ser Leu Leu Ser Val Thr

20 25 30

Trp Val Glu Glu Pro Cys Gly Pro Gly Pro Pro Gln Pro Gly Asp Ser

35 40 45

Glu Leu Pro Pro Arg Gly Asn Thr Asn Ala Ala Arg Arg Pro Asn Ser

50 55 60

Val Gln Pro Gly Ser Glu Arg Glu Arg Pro Gly Ala Gly Ala Gly Thr

65 70 75 80

Gly Glu Ser Trp Glu Pro Arg Val Leu Pro Tyr His Pro Ala Gln Pro
85 90 95

Gly Gln Ala Thr Lys Lys Ala Val Arg Thr Arg Tyr Ile Ser Thr Glu
100 105 110

Leu Gly Ile Arg Gln Lys Leu Leu Val Ala Val Leu Thr Ser Gln Ala
115 120 125

Thr Leu Pro Thr Leu Gly Val Ala Val Asn Arg Thr Leu Gly His Arg
130 135 140

Leu Glu His Val Val Phe Leu Thr Gly Ala Arg Gly Arg Arg Thr Pro
145 150 155 160

Ser Gly Met Ala Val Val Ala Leu Gly Glu Glu Arg Pro Ile Gly His
165 170 175

Leu His Leu Ala Leu Arg His Leu Leu Glu Gln His Gly Asp Asp Phe
180 185 190

Asp Trp Phe Phe Leu Val Pro Asp Ala Thr Tyr Thr Glu Ala His Gly
195 200 205

Leu Asp Arg Leu Ala Gly His Leu Ser Leu Ala Ser Ala Thr His Leu
210 215 220

Tyr Leu Gly Arg Pro Gln Asp Phe Ile Gly Gly Asp Thr Thr Pro Gly

225 230 235 240

230

235

240

Arg Tyr Cys His Gly Gly Phe Gly Val Leu Leu Ser Arg Thr Leu Leu
245 250 255

245

250

255

Gln Gln Leu Arg Pro His Leu Glu Ser Cys Arg Asn Asp Ile Val Ser
260 265 270

260

265

270

Ala Arg Pro Asp Glu Trp Leu Gly Arg Cys Ile Leu Asp Ala Thr Gly
275 280 285

275

280

285

Val Gly Cys Thr Gly Asp His Glu Gly Met His Tyr Asn Tyr Leu Glu
290 295 300

290

295

300

Leu Ser Pro Gly Glu Pro Val Gln Glu Gly Asp Pro Arg Phe Arg Ser
305 310 315 320

305

310

315

320

Ala Leu Thr Ala His Pro Val Arg Asp Pro Val His Met Tyr Gln Leu
325 330 335

325

330

335

His Lys Ala Phe Ala Arg Ala Glu Leu Asp Arg Thr Tyr Gln Glu Ile
340 345 350

340

345

350

Gln Glu Leu Gln Trp Glu Ile Gln Asn Thr Ser Arg Leu Ala Ala Asp
355 360 365

355

360

365

Gly Glu Arg Ala Ser Ala Trp Pro Val Gly Ile Pro Ala Pro Ser Arg
370 375 380

370

375

380

Pro Ala Ser Arg Phe Glu Val Leu Arg Trp Asp Tyr Phe Thr Glu Gln
385 390 395 400

Tyr Ala Phe Ser Cys Ala Asp Gly Ser Pro Arg Cys Pro Leu Arg Gly
405 410 415

Ala Asp Gln Ala Asp Val Ala Asp Val Leu Gly Thr Ala Leu Glu Glu
420 425 430

Leu Asn Arg Arg Tyr Gln Pro Ala Leu Gln Leu Gln Lys Gln Gln Leu
435 440 445

Val Asn Gly Tyr Arg Arg Phe Asp Pro Ala Arg Gly Met Glu Tyr Thr
450 455 460

Leu Asp Leu Gln Leu Glu Ala Leu Thr Pro Gln Gly Gly Arg Trp Pro
465 470 475 480

Leu Thr Arg Arg Val Gln Leu Leu Arg Pro Leu Ser Arg Val Glu Ile
485 490 495

Leu Pro Val Pro Tyr Val Thr Glu Ala Ser Arg Leu Thr Val Leu Leu
500 505 510

Pro Leu Ala Ala Ala Glu Arg Asp Leu Ala Ser Gly Phe Leu Glu Ala
515 520 525

Phe Ala Thr Ala Ala Leu Glu Pro Gly Asp Ala Ala Ala Leu Thr Leu
530 535 540

Leu Leu Leu Tyr Glu Pro Arg Gln Ala Gln Arg Ala Ala His Ser Asp
545 550 555 560

Val Phe Ala Pro Val Lys Ala His Val Ala Glu Leu Glu Arg Arg Phe
565 570 575

Pro Gly Ala Arg Val Pro Trp Leu Ser Val Gln Thr Ala Ala Pro Ser
580 585 590

Pro Leu Arg Leu Met Asp Leu Leu Ser Lys Lys His Pro Leu Asp Thr
595 600 605

Leu Phe Leu Leu Ala Gly Pro Asp Thr Val Leu Thr Pro Asp Phe Leu
610 615 620

Asn Arg Cys Arg Met His Ala Ile Ser Gly Trp Gln Ala Phe Phe Pro
625 630 635 640

Met His Phe Gln Ala Phe His Pro Ala Val Ala Pro Pro Gln Gly Pro
645 650 655

Gly Pro Pro Glu Leu Gly Arg Asp Thr Gly His Phe Asp Arg Gln Ala
660 665 670

Ala Ser Glu Ala Cys Phe Tyr Asn Ser Asp Tyr Val Ala Ala Arg Gly
675 680 685

Arg Leu Val Ala Ala Ser Glu Gln Glu Glu Glu Leu Leu Glu Ser Leu
690 695 700

Asp Val Tyr Glu Leu Phe Leu Arg Phe Ser Asn Leu His Val Leu Arg
705 710 715 720

Ala Val Glu Pro Ala Leu Leu Gln Arg Tyr Arg Ala Gln Pro Cys Ser
725 730 735

Ala Arg Leu Ser Glu Asp Leu Tyr His Arg Cys Arg Gln Ser Val Leu
740 745 750

Glu Gly Leu Gly Ser Arg Thr Gln Leu Ala Met Leu Leu Phe Glu Gln
755 760 765

Glu Gln Gly Asn Ser Thr
770

<210> 69
<211> 984
<212> DNA
<213> mouse

<220>
<221> CDS
<222> (1).. (984)
<223>

<400> 69

atg ttg ccc tcc cgg agg aaa gcg gcg cag ctg ccc tgg gag gat ggc	48
Met Leu Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly	
1 5 10 15	
agg gcc agg ttg ctt cct gga ggc ctc cgc cgg aaa tgc tcc atc ttc	96
Arg Ala Arg Leu Leu Pro Gly Gly Leu Arg Arg Lys Cys Ser Ile Phe	
20 25 30	
cac ctc ttc att gcc ttt ctc ctg ttg gtc ttc ttc tcc ctg ctc tgg	144
His Leu Phe Ile Ala Phe Leu Leu Leu Val Phe Phe Ser Leu Leu Trp	
35 40 45	
ctg cag ctc agc tgt tct gga gat atg gcc cag gtg acc agg gga caa	192
Leu Gln Leu Ser Cys Ser Gly Asp Met Ala Gln Val Thr Arg Gly Gln	
50 55 60	
ggg caa gag acc tcg ggt cca ccc cgg gct tgc cct cca gag ccg ccc	240
Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro	
65 70 75 80	
cct gag cac tgg gaa gaa gat gag tcc tgg ggg ccc cac cgc ttg gca	288
Pro Glu His Trp Glu Glu Asp Glu Ser Trp Gly Pro His Arg Leu Ala	
85 90 95	
gtg ctg gtg ccc ttt cgt gag cgc ttt gag gag ctg ctg gtc ttt gtg	336
Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val	
100 105 110	
ccc cac atg cac cgc ttc cta agc agg aag agg atc cag cac cac atc	384
Pro His Met His Arg Phe Leu Ser Arg Lys Arg Ile Gln His His Ile	
115 120 125	
tat gtg ctc aac cag gig gac cat ttc agg ttc aat cgg gca gca ctc	432
Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu	
130 135 140	
atc aat gtg ggc ttc ctg gag agc agc aac agc aca gac tac atc gcc	480
Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala	
145 150 155 160	
atg cac gat gtg gac ctg ctc cct ctc aat gag gag ctg gac tat ggc	528
Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly	
165 170 175	
ttc ccg gag gct ggg ccc ttc cat gtg gcc tcc cca gag ctc cac cct	576
Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro	

180	185	190	
ctc tac cac tac aag acc tat gtg ggc ggc att ctg ctg ctg tcc aaa			624
Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys			
195	200	205	
cag cac tac cag ctg tgc aac gga atg tcc aac cgc ttt tgg ggc tgg			672
Gln His Tyr Gln Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp			
210	215	220	
ggc cga gag gat gat gaa ttc tac cgg cgc atc aaa gga gct ggc ctc			720
Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu			
225	230	235	240
cag ctt ttc cgc ccc tgc gga atc aca act ggg tac cag aca ttt cgc			768
Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Gln Thr Phe Arg			
245	250	255	
cac ttg cat gac cct gcc tgg cgg aag agg gac caa aaa cgc att gcg			816
His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala			
260	265	270	
gct caa aaa cag gaa cag ttc aag gtg gac cgg gag gga ggc ctg aac			864
Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn			
275	280	285	
act gtg aag tac cgg gtg gat tcc cgc acg gca ctg tct ata gga ggg			912
Thr Val Lys Tyr Arg Val Asp Ser Arg Thr Ala Leu Ser Ile Gly Gly			
290	295	300	
gcc ccg tgc act gtc ctc aat gtc atg ctg gac tgc gat aaa aca gcc			960
Ala Pro Cys Thr Val Leu Asn Val Met Leu Asp Cys Asp Lys Thr Ala			
305	310	315	320
acc cca tgg tgc ata ttt ggc tga			984
Thr Pro Trp Cys Ile Phe Gly			
325			

<210> 70
 <211> 327
 <212> PRT
 <213> mouse

<400> 70

Met Leu Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp Gly

1 5 10 15

Arg Ala Arg Leu Leu Pro Gly Gly Leu Arg Arg Lys Cys Ser Ile Phe
20 25 30

His Leu Phe Ile Ala Phe Leu Leu Leu Val Phe Phe Ser Leu Leu Trp
35 40 45

Leu Gln Leu Ser Cys Ser Gly Asp Met Ala Gln Val Thr Arg Gly Gln
50 55 60

Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys Pro Pro Glu Pro Pro
65 70 75 80

Pro Glu His Trp Glu Glu Asp Glu Ser Trp Gly Pro His Arg Leu Ala
85 90 95

Val Leu Val Pro Phe Arg Glu Arg Phe Glu Glu Leu Leu Val Phe Val
100 105 110

Pro His Met His Arg Phe Leu Ser Arg Lys Arg Ile Gln His His Ile
115 120 125

Tyr Val Leu Asn Gln Val Asp His Phe Arg Phe Asn Arg Ala Ala Leu
130 135 140

Ile Asn Val Gly Phe Leu Glu Ser Ser Asn Ser Thr Asp Tyr Ile Ala
145 150 155 160

Met His Asp Val Asp Leu Leu Pro Leu Asn Glu Glu Leu Asp Tyr Gly
165 170 175

Phe Pro Glu Ala Gly Pro Phe His Val Ala Ser Pro Glu Leu His Pro
180 185 190

Leu Tyr His Tyr Lys Thr Tyr Val Gly Gly Ile Leu Leu Leu Ser Lys
195 200 205

Gln His Tyr Gln Leu Cys Asn Gly Met Ser Asn Arg Phe Trp Gly Trp
210 215 220

Gly Arg Glu Asp Asp Glu Phe Tyr Arg Arg Ile Lys Gly Ala Gly Leu
225 230 235 240

Gln Leu Phe Arg Pro Ser Gly Ile Thr Thr Gly Tyr Gln Thr Phe Arg
245 250 255

His Leu His Asp Pro Ala Trp Arg Lys Arg Asp Gln Lys Arg Ile Ala
260 265 270

Ala Gln Lys Gln Glu Gln Phe Lys Val Asp Arg Glu Gly Gly Leu Asn
275 280 285

Thr Val Lys Tyr Arg Val Asp Ser Arg Thr Ala Leu Ser Ile Gly Gly
290 295 300

Ala Pro Cys Thr Val Leu Asn Val Met Leu Asp Cys Asp Lys Thr Ala
305 310 315 320

Thr Pro Trp Cys Ile Phe Gly
325